

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/524,619
Source: PT
Date Processed by STIC: 3/3/06

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 03/03/2006

PATENT APPLICATION: US/10/524,619

TIME: 12:54:53

Input Set : A:\DAVI251.001APC sequence listing.TXT

Output Set: N:\CRF4\03032006\J524619.raw

3 <110> APPLICANT: Melbourne Health
4 Jane, Stephen (US Only)
5 Wilanowski, Tomasz (US only)
6 Ting, Stephen (US only)
8 <120> TITLE OF INVENTION: MAMMALIAN GRAINYHEAD TRANSCRIPTION FACTORS
10 <130> FILE REFERENCE: DAVI251.001APC
12 <140> CURRENT APPLICATION NUMBER: US 10/524,619
13 <141> CURRENT FILING DATE: 2005-02-09
15 <150> PRIOR APPLICATION NUMBER: PCT/AU03/01006
16 <151> PRIOR FILING DATE: 2003-08-08
18 <150> PRIOR APPLICATION NUMBER: US 60/402055
19 <151> PRIOR FILING DATE: 2002-08-09
21 <150> PRIOR APPLICATION NUMBER: AU2002951579
22 <151> PRIOR FILING DATE: 2002-08-22
24 <160> NUMBER OF SEQ ID NOS: 46
26 <170> SOFTWARE: PatentIn version 3.1
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 1881
30 <212> TYPE: DNA
31 <213> ORGANISM: human
33 <220> FEATURE:
34 <221> NAME/KEY: CDS
35 <222> LOCATION: (94)..(1323)
38 <400> SEQUENCE: 1
39 ataagagagg ccatctgaca gctccagata cgacagtcac tgtctccata gcaacgatgc
41 ctaccactc catcaagaca gaaacccagc cac atg gct tcg ctg tgg gaa tcc
42 Met Ala Ser Leu Trp Glu Ser
43 1 5
45 ccc cag cag tgt atc atc ctg agc cca ctg agc ggg tgg tgg ttt tcg
46 Pro Gln Gln Cys Ile Ile Leu Ser Pro Leu Ser Gly Trp Trp Phe Ser
47 10 15 20
49 atc gga atc tca ata ctg acc agt tca gct ctg gtg ctc aag ccc caa
50 Ile Gly Ile Ser Ile Leu Thr Ser Ser Ala Leu Val Leu Lys Pro Gln
51 25 30 35
53 atg ctc aaa ggc gaa ctc cag act cga cct tct cag aga cct tca agg
54 Met Leu Lys Gly Glu Leu Gln Thr Arg Pro Ser Gln Arg Pro Ser Arg
55 40 45 50 55
57 aag gcg ttc agg agg aac aac ttt gaa tat acc cta gaa gct tca aaa
58 Lys Ala Phe Arg Arg Asn Asn Phe Glu Tyr Thr Leu Glu Ala Ser Lys
59 60 65 70
61 tca ctt cga cag aag cca gga gac agt acc atg acg tac ctg aac aaa
62 Ser Leu Arg Gln Lys Pro Gly Asp Ser Thr Met Thr Tyr Leu Asn Lys
63 75 80 85

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65 ggc cag ttc tat ccc atc acc ttg aag gag gtg agc agc agt gaa gga	402
66 Gly Gln Phe Tyr Pro Ile Thr Leu Lys Glu Val Ser Ser Ser Glu Gly	
67 90 95 100	
69 atc cat cat ccc atc agc aaa gtt cga agt gtg atc atg gtg gtt ttt	450
70 Ile His His Pro Ile Ser Lys Val Arg Ser Val Ile Met Val Val Phe	
71 105 110 115	
73 gct gaa gac aaa agc aga gaa gat cag tta agg cat tgg aag tac tgg	498
74 Ala Glu Asp Lys Ser Arg Glu Asp Gln Leu Arg His Trp Lys Tyr Trp	
75 120 125 130 135	
77 cac tcc cgg cag cac acc gct aaa caa aga tgc att gac ata gct gac	546
78 His Ser Arg Gln His Thr Ala Lys Gln Arg Cys Ile Asp Ile Ala Asp	
79 140 145 150	
81 tat aaa gaa agc ttc aac act atc agt aac atc gag gag att gcg tat	594
82 Tyr Lys Glu Ser Phe Asn Thr Ile Ser Asn Ile Glu Glu Ile Ala Tyr	
83 155 160 165	
85 aac gcc att tcc ttc aca tgg gac atc aac gat gaa gca aag gtt ttc	642
86 Asn Ala Ile Ser Phe Thr Trp Asp Ile Asn Asp Glu Ala Lys Val Phe	
87 170 175 180	
89 atc tct gtc aac tgc tta aca gat ttc tct tcc cag aag gga gtg	590
90 Ile Ser Val Asn Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys Gly Val	
91 185 190 195	
93 aag ggg ttg cct ctt aac att caa gtt gat acc tat agt tac aac aac	738
94 Lys Gly Leu Pro Leu Asn Ile Gln Val Asp Thr Tyr Ser Tyr Asn Asn	
95 200 205 210 215	
97 cgc agc aac aag cct gtg cac cgg gcc tac tgc cag atc aag gtc ttc	786
98 Arg Ser Asn Lys Pro Val His Arg Ala Tyr Cys Gln Ile Lys Val Phe	
99 220 225 230	
101 tgt gac aag gga gct gag cgg aaa atc agg gat gaa gaa cga aag caa	834
102 Cys Asp Lys Gly Ala Glu Arg Lys Ile Arg Asp Glu Glu Arg Lys Gln	
103 235 240 245	
105 agc aaa aga aaa gtt tct gat gtt aaa gtg cca ctg ctt ccc tct cac	882
106 Ser Lys Arg Lys Val Ser Asp Val Lys Val Pro Leu Leu Pro Ser His	
107 250 255 260	
109 aag cga atg gat atc aca gtt ttc aaa ccc ttc att gat ctc gat act	930
110 Lys Arg Met Asp Ile Thr Val Phe Lys Pro Phe Ile Asp Leu Asp Thr	
111 265 270 275	
113 cag cct gtc ctc ttc att cct gac gtg cac ttt gcc aac ttg cag cgg	978
114 Gln Pro Val Leu Phe Ile Pro Asp Val His Phe Ala Asn Leu Gln Arg	
115 280 285 290 295	
117 ggc act cat gtc ctt ccc att gcc tct gaa gaa ttg gag ggt gaa ggc	1026
118 Gly Thr His Val Leu Pro Ile Ala Ser Glu Glu Leu Glu Gly Glu Gly	
119 300 305 310	
121 tct gtc ttg aaa agg ggg ccg tac ggc aca gaa gat gac ttt gct gtc	1074
122 Ser Val Leu Lys Arg Gly Pro Tyr Gly Thr Glu Asp Asp Phe Ala Val	
123 315 320 325	
125 cct cct tct acc aag ctg gcc cgg ata gaa gaa cca aag aga gtg ctg	1122
126 Pro Pro Ser Thr Lys Leu Ala Arg Ile Glu Glu Pro Lys Arg Val Leu	
127 330 335 340	
129 ctc tac gtt cga aag gag tca gaa gaa gtc ttt gat gcc ctg atg ctc	1170

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130	Leu	Tyr	Val	Arg	Lys	Glu	Ser	Glu	Glu	Val	Phe	Asp	Ala	Leu	Met	Leu	
131	345						350						355				
133	aaa	acc	cca	tct	ttg	aag	ggc	ttg	atg	gaa	gct	atc	tca	gac	aaa	tac	1218
134	Lys	Thr	Pro	Ser	Leu	Lys	Gly	Leu	Met	Glu	Ala	Ile	Ser	Asp	Lys	Tyr	
135	360						365					370			375		
137	gat	gtt	ccc	cat	gac	aag	att	ggg	aaa	ata	ttc	aag	aag	tgt	aaa	aag	1266
138	Asp	Val	Pro	His	Asp	Lys	Ile	Gly	Ile	Phe	Lys	Lys	Cys	Lys	Lys		
139							380				385			390			
141	ggg	atc	ctg	gtg	aac	atg	gac	gac	aac	att	gtg	aag	cat	tac	tcc	aat	1314
142	Gly	Ile	Leu	Val	Asn	Met	Asp	Asp	Asn	Ile	Val	Lys	His	Tyr	Ser	Asn	
143							395				400			405			
145	gag	gac	acc	ttccagctgc	agattgaaga	agccgggggg	tcttacaagc										1363
146	Glu	Asp	Thr														
147			410														
149	tcaccctgac	ggagatctaa	aggcctgcgg	gccacagctc	cccaggagtt	cagtgcaggt											1423
151	gtttctagat	cttacggttt	ggcaactgca	ggtaacccca	gtcagccatg	tcgcccagcac											1483
153	aggtctatgt	cgagggaaatg	ggttccttgc	aggttggagg	cggggctgca	tctggcttgg											1543
155	tggtagcatt	taatctattt	cattggtgtt	tttcagatga	aagagaaatc	catataccat											1603
157	tatgtttgaa	tttctgtata	tatacaggat	tttacagtgaa	aactttatc	caagagttaa											1663
159	cagagtctct	gggaagctt	aggacatctg	ctacgttatt	tatcaaata	ttgggatctc											1723
161	tgccttgc	ctacagtgtc	gtgggcctgc	tcgctagcag	aagtcagaaa	aggcgatagg											1783
163	cttggcttta	aggatttcgt	gcccttgcct	gaattcagta	caactccact	gcctcacgtt											1843
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169	<211>	LENGTH:	410														
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176	1				5				10					15			
179	Leu	Ser	Gly	Trp	Trp	Phe	Ser	Ile	Gly	Ile	Ser	Ile	Leu	Thr	Ser	Ser	
180					20				25				30				
183	Ala	Leu	Val	Leu	Lys	Pro	Gln	Met	Leu	Lys	Gly	Glu	Leu	Gln	Thr	Arg	
184					35				40			45					
187	Pro	Ser	Gln	Arg	Pro	Ser	Arg	Lys	Ala	Phe	Arg	Arg	Asn	Asn	Phe	Glu	
188					50				55			60					
191	Tyr	Thr	Leu	Glu	Ala	Ser	Lys	Ser	Leu	Arg	Gln	Lys	Pro	Gly	Asp	Ser	
192					65				70			75			80		
195	Thr	Met	Thr	Tyr	Leu	Asn	Lys	Gly	Gln	Phe	Tyr	Pro	Ile	Thr	Leu	Lys	
196					85				90			95					
199	Glu	Val	Ser	Ser	Ser	Glu	Gly	Ile	His	His	Pro	Ile	Ser	Lys	Val	Arg	
200					100				105			110					
203	Ser	Val	Ile	Met	Val	Val	Phe	Ala	Glu	Asp	Lys	Ser	Arg	Glu	Asp	Gln	
204					115				120			125					
207	Leu	Arg	His	Trp	Lys	Tyr	Trp	His	Ser	Arg	Gln	His	Thr	Ala	Lys	Gln	
208					130				135			140					
211	Arg	Cys	Ile	Asp	Ile	Ala	Asp	Tyr	Lys	Glu	Ser	Phe	Asn	Thr	Ile	Ser	
212	145				145				150			155			160		
215	Asn	Ile	Glu	Glu	Ile	Ala	Tyr	Asn	Ala	Ile	Ser	Phe	Thr	Trp	Asp	Ile	

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216	165	170	175	
219	Asn Asp Glu Ala Lys Val Phe Ile Ser Val Asn Cys Leu Ser Thr Asp			
220	180	185	190	
223	Phe Ser Ser Gln Lys Gly Val Lys Gly Leu Pro Leu Asn Ile Gln Val			
224	195	200	205	
227	Asp Thr Tyr Ser Tyr Asn Asn Arg Ser Asn Lys Pro Val His Arg Ala			
228	210	215	220	
231	Tyr Cys Gln Ile Lys Val Phe Cys Asp Lys Gly Ala Glu Arg Lys Ile			
232	225	230	235	240
235	Arg Asp Glu Glu Arg Lys Gln Ser Lys Arg Lys Val Ser Asp Val Lys			
236	245	250	255	
239	Val Pro Leu Leu Pro Ser His Lys Arg Met Asp Ile Thr Val Phe Lys			
240	260	265	270	
243	Pro Phe Ile Asp Leu Asp Thr Gln Pro Val Leu Phe Ile Pro Asp Val			
244	275	280	285	
247	His Phe Ala Asn Leu Gln Arg Gly Thr His Val Leu Pro Ile Ala Ser			
248	290	295	300	
251	Glu Glu Leu Glu Gly Glu Gly Ser Val Leu Lys Arg Gly Pro Tyr Gly			
252	305	310	315	320
255	Thr Glu Asp Asp Phe Ala Val Pro Pro Ser Thr Lys Leu Ala Arg Ile			
256	325	330	335	
259	Glu Glu Pro Lys Arg Val Leu Leu Tyr Val Arg Lys Glu Ser Glu Glu			
260	340	345	350	
263	Val Phe Asp Ala Leu Met Leu Lys Thr Pro Ser Leu Lys Gly Leu Met			
264	355	360	365	
267	Glu Ala Ile Ser Asp Lys Tyr Asp Val Pro His Asp Lys Ile Gly Lys			
268	370	375	380	
271	Ile Phe Lys Lys Cys Lys Lys Gly Ile Leu Val Asn Met Asp Asp Asn			
272	385	390	395	400
275	Ile Val Lys His Tyr Ser Asn Glu Asp Thr			
276	405	410		
279	<210> SEQ ID NO: 3			
280	<211> LENGTH: 2361			
281	<212> TYPE: DNA			
282	<213> ORGANISM: human			
284	<220> FEATURE:			
285	<221> NAME/KEY: CDS			
286	<222> LOCATION: (7)..(1860)			
288	<220> FEATURE:			
289	<221> NAME/KEY: VARIANT			
290	<222> LOCATION: 342			
291	<223> OTHER INFORMATION: Xaa = Lys, Ile			
294	<400> SEQUENCE: 3			
295	agcgcg atg aca cag gag tac gac aac aaa cgg cca gtg ttg gtt ctt		48	
296	Met Thr Gln Glu Tyr Asp Asn Lys Arg Pro Val Leu Val Leu			
297	1	5	10	
299	cag aat gaa gca ctt tat cca cag cgg cgg tcc tac act agt gag gat			
300	Gln Asn Glu Ala Leu Tyr Pro Gln Arg Arg Ser Tyr Thr Ser Glu Asp			
301	15	20	25	30

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303 gag gcc tgg aaa tcc ttc ctg gaa aac cct ctc act gca gcg acc aaa	144
304 Glu Ala Trp Lys Ser Phe Leu Glu Asn Pro Leu Thr Ala Ala Thr Lys	
305 35 40 45	
307 gcg atg atg agc atc aat gga gat gaa gac agc gcc gct gcg ctg ggc	192
308 Ala Met Met Ser Ile Asn Gly Asp Glu Asp Ser Ala Ala Ala Leu Gly	
309 50 55 60	
311 ctg ctc tat gac tac tac aag gtt cca aga gag aga agg tca tca aca	240
312 Leu Leu Tyr Asp Tyr Tyr Lys Val Pro Arg Glu Arg Arg Ser Ser Thr	
313 65 70 75	
315 gca aag cca gag gtg gag cac cct gag cca gat cac agc aaa aga aac	288
316 Ala Lys Pro Glu Val Glu His Pro Glu Pro Asp His Ser Lys Arg Asn	
317 80 85 90	
319 agc ata cca att gtg aca gag cag ccc ctc atc tct gct gga gaa aac	336
320 Ser Ile Pro Ile Val Thr Glu Gln Pro Leu Ile Ser Ala Gly Glu Asn	
321 95 100 105 110	
323 aga gtg caa gta ctg aaa aat gtg cca ttt aac att gtc ctt ccc cat	384
324 Arg Val Gln Val Leu Lys Asn Val Pro Phe Asn Ile Val Leu Pro His	
325 115 120 125	
327 ggc aac cag ctg ggc att gat aag aga ggc cat ctg aca gct tca gat	432
328 Gly Asn Gln Leu Gly Ile Asp Lys Arg Gly His Leu Thr Ala Ser Asp	
329 130 135 140	
331 acg aca gtc act gtc tcc ata gca acg atg cct acc cac tcc atc aag	480
332 Thr Thr Val Thr Val Ser Ile Ala Thr Met Pro Thr His Ser Ile Lys	
333 145 150 155	
335 aca gaa acc cag cca cat ggc ttc gct gtg gga atc ccc cca gca gtg	528
336 Thr Glu Thr Gln Pro His Gly Phe Ala Val Gly Ile Pro Pro Ala Val	
337 160 165 170	
339 tat cat cct gag ccc act gag cgg gtg gtt ttc gat cgg aay ctc	576
340 Tyr His Pro Glu Pro Thr Glu Arg Val Val Phe Asp Arg Asn Leu	
341 175 180 185 190	
343 aat act gac cag ttc agc tct ggt gct caa gcc cca aat gct caa agg	624
344 Asn Thr Asp Gln Phe Ser Ser Gly Ala Gln Ala Pro Asn Ala Gln Arg	
345 195 200 205	
347 cga act cca gac tcg acc ttc tca gag acc ttc aag gaa ggc gtt cag	672
348 Arg Thr Pro Asp Ser Thr Phe Ser Glu Thr Phe Lys Glu Gly Val Gln	
349 210 215 220	
351 gag gtt ttc ccc tcg gat ctc agt ctg cgg atg cct ggc atg aat	720
352 Glu Val Phe Phe Pro Ser Asp Leu Ser Leu Arg Met Pro Gly Met Asn	
353 225 230 235	
355 tca gag gac tat gtt ttt gac agt gtt tct ggg aac aac ttt gaa tat	768
356 Ser Glu Asp Tyr Val Phe Asp Ser Val Ser Gly Asn Asn Phe Glu Tyr	
357 240 245 250	
359 acc cta gaa gct tca aaa tca ctt cga cag aag cca gga gac agt acc	816
360 Thr Leu Glu Ala Ser Lys Ser Leu Arg Gln Lys Pro Gly Asp Ser Thr	
361 255 260 265 270	
363 atg acg tac ctg aac aaa ggc cag ttc tat ccc atc acc ttg aag gag	864
364 Met Thr Tyr Leu Asn Lys Gly Gln Phe Tyr Pro Ile Thr Leu Lys Glu	
365 275 280 285	
367 gtg agc agc agt gaa gga atc cat cat ccc atc agc aaa gtt cga agt	912

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; Xaa Pos. 342
Seq#:4; Xaa Pos. 342
Seq#:7; Xaa Pos. 117,172
Seq#:8; Xaa Pos. 117,172'
Seq#:9; N Pos. 2634,2968
Seq#:11; N Pos. 2973,3307-
Seq#:15; N Pos. 2806

VERIFICATION SUMMARY

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L:380 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:1056
L:566 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:336
L:1121 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:439
L:1133 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:583
L:1290 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:112
L:1302 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:160
L:1518 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:2580
L:1530 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:2940
L:1796 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:2940
L:1808 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:3300
L:2427 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:2788